

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Bandman, Olga
Lal, Preeti
Shah, Purvi

(ii) TITLE OF THE INVENTION: NEW HUMAN INTEGRAL MEMBRANE PROTEIN

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0339 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BRAINOT03
(B) CLONE: 662708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met Val Lys Ile Ser Phe Gln Pro Ala Val Ala Gly Ile Lys Gly Asp
 1           5           10           15
Lys Ala Asp Lys Ala Ser Ala Ser Ala Pro Ala Pro Ala Ser Ala Thr
          20           25           30
Glu Ile Leu Leu Thr Pro Ala Arg Glu Glu Gln Pro Pro Gln His Arg
          35           40           45
Ser Lys Arg Gly Gly Ser Val Gly Gly Val Cys Tyr Leu Ser Met Gly
          50           55           60
Met Val Val Leu Leu Met Gly Leu Val Phe Ala Ser Val Tyr Ile Tyr

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0965710-03099

65 70 75 80
 Arg Tyr Phe Phe Leu Ala Gln Leu Ala Arg Asp Asn Phe Phe Arg Cys
 85 90 95
 Gly Val Leu Tyr Glu Asp Ser Leu Ser Gln Val Arg Thr Gln Met
 100 105 110
 Glu Leu Glu Glu Asp Val Lys Ile Tyr Leu Asp Glu Asn Tyr Glu Arg
 115 120 125
 Ile Asn Val Pro Val Pro Gln Phe Gly Gly Gly Asp Pro Ala Asp Ile
 130 135 140
 Ile His Asp Phe Gln Arg Gly Leu Thr Ala Tyr His Asp Ile Leu Asp
 145 150 155 160
 Lys Cys Tyr Val Ile Glu Leu Asn Thr Thr Ile Val Leu Pro Pro Arg
 165 170 175
 Asn Phe Trp Glu Leu Leu Met Asn Val Lys Arg Gly Thr Tyr Leu Pro
 180 185 190
 Gln Thr Tyr Ile Ile Gln Glu Glu Met Val Val Thr Glu His Val Ser
 195 200 205
 Asp Lys Glu Ala Leu Gly Ser Phe Ile Tyr His Leu Cys Asn Gly Lys
 210 215 220
 Asp Thr Tyr Arg Leu Arg Arg Arg Ala Thr Arg Arg Arg Ile Asn Lys
 225 230 235 240
 Arg Gly Ala Lys Asn Cys Asn Ala Ile Arg His Phe Glu Asn Thr Phe
 245 250 255
 Val Val Glu Thr Leu Ile Cys Gly Val Val
 260 265

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) BRAINOT03
 (B) CLONE: 662708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGAGCGGGAT	CCAAACTTCC	GGTGCCTGCA	GAGCTCGGAG	CGGCGGAGGC	AGAGACCGAG	60
GCTGCACCGG	CAGAGGCTGC	GGGGCGGACG	CGCGGGCCGG	CGCAGCCATG	GTGAAGATTA	120
GCTTCCAGCC	CGCCGTGGCT	GGCATCAAGG	GCGACAAGGC	TGACAAGGCG	TCGGCGTCGG	180
CCCCTGCGCC	GGCCTCGGCC	ACCGAGATCC	TGCTGACGCC	GGCTAGGGAG	GAGCAGCCCC	240
CACAACATCG	ATCCAAGAGG	GGGGGCTCAG	TGGGCGGCGT	GTGCTACCTG	TCGATGGGCA	300
TGGTCGTGCT	GCTCATGGGC	CTCGTGTTCT	CCTCTGTCTA	CATCTACAGA	TACTTCTTTC	360
TTGCACAGCT	GGCCCGAGAT	AACTTCTTCC	GCTGTGGTGT	GCTGTATGAG	GACTCCCTGT	420
CCTCCCAGGT	CCGGACTCAG	ATGGAGCTGG	AAGAGGATGT	GAAAATCTAC	CTCGACGAGA	480
ACTACGAGCG	CATCAACGTG	CCTGTGCCCC	AGTTTGGCGG	CGGTGACCCT	GCAGACATCA	540
TCCATGACTT	CCAGCGGGGT	CTGACTGCGT	ACCATGATAT	CTTGGACAAG	TGCTATGTCA	600
TCGAACCTAA	CACCACCATT	GTGCTGCCCC	CTCGCAACTT	CTGGGAGCTC	CTCATGAACG	660
TGAAGAGGGG	GACCTACCTG	CCGCAGACGT	ACATCATCCA	GGAGGAGATG	GTGGTCACGG	720
AGCATGTGAG	TGACAAGGAG	GCCCTGGGGT	CCTTCATCTA	CCACCTGTGC	AACGGGAAAG	780
ACACCTACCG	GCTCCGGGCG	CGGGCAACGC	GGAGGCGGAT	CAACAAGCGT	GGGGCCAAGA	840
ACTGCAATGC	CATCCGCCAC	TTCGAGAACA	CCTTCGTGGT	GGAGACGCTC	ATCTGCGGGG	900
TGGTGTGAGG	CCCTCCTCCC	CCAGAACCCC	CTGCCGTGTT	CCTCTTTTCT	TCTTTCCGGC	960
TGCTCTCTGG	CCCTCCTCCT	TCCCCCTGCT	TAGCTTGATC	TTTGGACGCG	TTTCTATAGA	1020
GGTGACATGT	CTCTCCATTC	CTCTCCAACC	CTGCCACCT	CCCTGTACCA	GAGCTGTGAT	1080
CTCTCGGTGG	GGGGCCCATC	TCTGCTGACC	TGGGTGTGGC	GGAGGGAGAG	GCGATGCTGC	1140
AAAGTGTTTT	CTGTGTCCCA	CTGTCTTGAA	GCTGGGCCTG	C		1181

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 624778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Val	Lys	Ile	Ala	Phe	Asn	Thr	Pro	Thr	Ala	Val	Gln	Lys	Glu	Glu	1	5	10	15
Ala	Arg	Gln	Asp	Ile	Glu	Ala	Leu	Val	Ser	Arg	Thr	Val	Arg	Ala	Gln	20	25	30	
Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Val	Pro	Gln	Glu	Lys	Asp	Gly	35	40	45	
Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu	Ser	Phe	Ile	Leu	50	55	60	
Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr	Lys	Tyr	Phe	Met	Pro	65	70	75	80
Lys	Ser	Thr	Ile	Tyr	His	Gly	Glu	Met	Cys	Phe	Phe	Asp	Ser	Glu	Asp	85	90	95	
Pro	Val	Asn	Ser	Ile	Pro	Gly	Gly	Glu	Pro	Tyr	Phe	Leu	Pro	Val	Thr	100	105	110	
Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp	Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	115	120	125	
Pro	Val	Pro	Ser	Phe	Ser	Asp	Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	130	135	140	
Phe	Glu	Lys	Gly	Met	Thr	Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	145	150	155	160
Tyr	Leu	Met	Pro	Leu	Asn	Thr	Ser	Ile	Val	Met	Thr	Pro	Lys	Asn	Leu	165	170	175	
Val	Glu	Leu	Phe	Gly	Lys	Leu	Ala	Ser	Gly	Lys	Tyr	Leu	Pro	His	Thr	180	185	190	
Tyr	Val	Val	Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	195	200	205	
Ser	Asn	Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	210	215	220	
Phe	Arg	Leu	Arg	Arg	Arg	Asp	Leu	Leu	Leu	Gly	Phe	Asn	Lys	Arg	Ala	225	230	235	240
Ile	Asp	Lys	Cys	Trp	Lys	Ile	Arg	His	Phe	Pro	Asn	Glu	Phe	Ile	Val	245	250	255	
Glu	Thr	Lys	Ile	Cys	Gln	Glu										260			